

SEQUENCE LISTING

Leu Phe Ala Pro Ser Tyr Thr Glu Thr His Tyr Thr Ser Ser Gly Asn
 20 25 30
 Pro Gln Thr Thr Thr Arg Lys Leu Glu Asp His Cys Phe Tyr His Gly
 35 40 45
 Thr Val Arg Glu Thr Glu Leu Ser Ser Val Thr Leu Ser Thr Cys Arg
 50 55 60
 Gly Ile Arg Gly Leu Ile Thr Val Ser Ser Asn Leu Ser Tyr Val Ile
 65 70 75 80
 Glu Pro Leu Pro Asp Ser Lys Gly Gln His Leu Ile Tyr Arg Ser Glu
 85 90 95
 His Leu Lys Pro Pro Pro Leu Thr Gly Arg Glu Val Leu Thr Pro Phe
 100 105 110
 Pro Gly Leu Gly Thr Ala Ala Ala Pro Ala Gln Gly Gly Ala His Leu
 115 120 125
 Lys Gln Cys Asp Leu Leu Lys Leu Ser Arg Arg Gln Lys Gln Leu Cys
 130 135 140
 Arg Arg Glu Pro Gly Leu Ala Glu Thr Leu Arg Asp Ala Ala His Leu
 145 150 155 160
 Gly Leu Leu Glu Cys Gln Phe Gln Phe Arg His Glu Arg Trp Asn Cys
 165 170 175
 Ser Leu Glu Gly Arg Met Gly Leu Leu Lys Arg Gly Phe Lys Glu Thr
 180 185 190
 Ala Phe Leu Tyr Ala Val Ser Ser Ala Ala Leu Thr His Thr Leu Ala
 195 200 205
 Arg Ala Cys Ser Ala Gly Arg Met Glu Arg Cys Thr Cys Asp Asp Ser
 210 215 220
 Pro Gly Leu Glu Ser Arg Gln Ala Trp Gln Trp Gly Val Cys Gly Asp
 225 230 235 240
 Asn Leu Lys Tyr Ser Thr Lys Phe Leu Ser Asn Phe Leu Gly Ser Lys
 245 250 255
 Arg Gly Asn Lys Asp Leu Arg Ala Arg Ala Asp Ala His Asn Thr His
 260 265 270
 Val Gly Ile Lys Ala Val Lys Ser Gly Leu Arg Thr Thr Cys Lys Cys
 275 280 285
 His Gly Val Ser Gly Ser Cys Ala Val Arg Thr Cys Trp Lys Gln Leu
 290 295 300
 Ser Pro Phe Arg Glu Thr Gly Gln Val Leu Lys Leu Arg Tyr Asp Ser
 305 310 315 320
 Ala Val Lys Val Ser Ser Ala Thr Asn Glu Ala Leu Gly Arg Leu Glu
 325 330 335
 Leu Trp Ala Pro Ala Arg Gln Gly Ser Leu Thr Lys Gly Leu Ala Pro
 340 345 350
 Arg Ser Gly Asp Leu Val Tyr Met Glu Asp Ser Pro Ser Phe Cys Arg
 355 360 365
 Pro Ser Lys Tyr Ser Pro Gly Thr Ala Gly Arg Val Cys Ser Arg Glu
 370 375 380
 Ala Ser Cys Ser Ser Leu Cys Cys Gly Arg Gly Tyr Asp Thr Gln Ser
 385 390 395 400
 Arg Leu Val Ala Phe Ser Cys His Cys Gln Val Gln Trp Cys Cys Tyr
 405 410 415
 Val Glu Cys Gln Gln Cys Val Gln Glu Leu Val Tyr Thr Cys Lys
 420 425 430
 His

195	200	205
Lys Ser Gly Leu Arg Thr	Thr Cys Lys Cys His	Gly Val Ser Gly Ser
210	215	220
Cys Ala Val Arg Thr	Cys Trp Lys Gln Leu Ser Pro	Phe Arg Glu Thr
225	230	235
Gly Gln Val Leu Lys Leu Arg Tyr Asp Ser Ala Val Lys Val Ser Ser		
245	250	255
Ala Thr Asn Glu Ala Leu Gly Arg	Leu Glu Leu Trp Ala Pro Ala Arg	
260	265	270
Gln Gly Ser Leu Thr Lys Gly Leu Ala Pro Arg Ser Gly Asp Leu Val		
275	280	285
Tyr Met Glu Asp Ser Pro Ser Phe Cys Arg Pro Ser Lys Tyr Ser Pro		
290	295	300
Gly Thr Ala Gly Arg Val Cys Ser Arg Glu Ala Ser Cys Ser Ser Leu		
305	310	315
Cys Cys Gly Arg Gly Tyr Asp Thr Gln Ser Arg Leu Val Ala Phe Ser		
325	330	335
Cys His Cys Gln Val Gln Trp Cys Cys Tyr Val Glu Cys Gln Gln Cys		
340	345	350
Val Gln Glu Leu Val Tyr Thr Cys Lys His		
355	360	

<210> 5
<211> 1726
<212> DNA
<213> homo sapiens

agcatccccca accttggta ggacttggag aggagggcag agtgag

1726

<210> 6

<211> 255

<212> DNA

<213> homo sapiens

<400> 6

atgttcagg ccctatccctg tgccatcccc aaagggttc ttccttact aacgggtta
gaagaggcta cgtgttgc agaaaaattt tctttgagga ccagcactca ccatcaagtt
catgttgggg gccaaacctg tccacctaag tgcccttgc caacacactt ctaccactgg
gaatctgtac aaaaagagga gaatgtgat tattctaaca ctttgaggat aggaagaggc
atcaataaaa cctga

60

120

180

240

255

<210> 7

<211> 84

<212> PRT

<213> homo sapiens

<400> 7

Met Phe Arg Ala Leu Ser Cys Ala Ile Pro Lys Gly Leu Leu Ser Leu
1 5 10 15
Leu Ser Arg Val Glu Glu Ala Thr Cys Cys Ile Glu Lys Leu Ser Leu
20 25 30
Arg Thr Ser Thr His His Gln Val His Val Glu Gly Gln Thr Cys Pro
35 40 45
Pro Lys Cys Leu Cys Thr Thr His Phe Tyr His Trp Glu Ser Val Gln
50 55 60
Lys Glu Glu Asn Val Ser Tyr Ser Asn Thr Leu Arg Ile Gly Arg Gly
65 70 75 80
Ile Asn Lys Thr

<210> 8

<211> 476

<212> DNA

<213> homo sapiens

<400> 8

cattgtgccc ggctgataat tcttacagtt tctttactc cctggccact cttggaggat
ctatgtccat tcttagatgtt cagggcccta tctctgtcoca tccccaaagg gcttcttcc
ttactaagca ggtagaaga ggctacgtgt tgcatagaga aattgtctt gaggaccagc
actcaccate aagttcatgt tgaggccaa acctgtccac cttaatgtcct ttgcaccaca
cacttttacc actggaaatc tgacaaaaa gaggagaatg tgatgttttc taactcttg
aggataggaa gaggcatcaa taaaacctga attccatcac aatgttttg caataaggcc
agactccctc ccaagacatt ccctttaagc cttgtatgttt tatctgtaaa gtgagaagag
tgatatcttcc ttccacaaggt tgatggaaa ataaaaatgac atacccgtccc gggccg

60

120

180

240

300

360

420

476